

Sequence Listing

<110> Baker, Kevin
Botstein, David
Eaton, Dan
Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljamin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William

<120> SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME

<130> P2548P1C1

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<213> Homo Sapien

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35 40 45
Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
50 55 60
Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
65 70 75
Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
80 85 90
Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
95 100 105
Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
110 115 120
Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
125 130 135
Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
140 145 150
Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
155 160 165
Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
170 175 180
Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
185 190 195
Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
200 205 210

Ile Glu Pro Gly	Ala Phe Glu Gly Val	Thr Val Phe His Ile Arg
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Ile Ala Glu Ala	Lys Leu Thr Ser Val	Pro Lys Gly Leu Pro Pro
230		240
Thr Leu Leu Glu	Leu His Leu Asp Tyr	Asn Lys Ile Ser Thr Val
245		255
Glu Leu Glu Asp	Phe Lys Arg Tyr Lys	Glu Leu Gln Arg Leu Gly
260		270
Leu Gly Asn Asn	Lys Ile Thr Asp Ile	Glu Asn Gly Ser Leu Ala
275		285
Asn Ile Pro Arg	Val Arg Glu Ile His	Leu Glu Asn Asn Lys Leu
290		300
Lys Lys Ile Pro	Ser Gly Leu Pro Glu	Leu Lys Tyr Leu Gln Ile
305		315
Ile Phe Leu His	Ser Asn Ser Ile Ala	Arg Val Gly Val Asn Asp
320		330
Phe Cys Pro Thr	Val Pro Lys Met Lys	Lys Ser Leu Tyr Ser Ala
335		345
Ile Ser Leu Phe	Asn Asn Pro Val Lys	Tyr Trp Glu Met Gln Pro
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Asn Phe Gly Met		

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<213> Homo Sapien

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65 70 75

Arg Cys Val Leu Cys	Ala Cys Glu Ala	Pro Gln Trp Gly Arg Arg	80	85	90
Thr Arg Gly Pro Gly	Arg Val Ser Cys	Lys Asn Ile Lys Pro Glu	95	100	105
Cys Pro Thr Pro Ala	Cys Gly Gln Pro	Arg Gln Leu Pro Gly His	110	115	120
Cys Cys Gln Thr Cys	Pro Gln Glu Arg	Ser Ser Ser Glu Arg Gln	125	130	135
Pro Ser Gly Leu Ser	Phe Glu Tyr Pro	Arg Asp Pro Glu His Arg	140	145	150
Ser Tyr Ser Asp Arg	Gly Glu Pro Gly	Ala Glu Glu Arg Ala Arg	155	160	165
Gly Asp Gly His Thr	Asp Phe Val Ala	Leu Leu Thr Gly Pro Arg	170	175	180
Ser Gln Ala Val Ala	Arg Ala Arg Val	Ser Leu Leu Arg Ser Ser	185	190	195
Leu Arg Phe Ser Ile	Ser Tyr Arg Arg	Leu Asp Arg Pro Thr Arg	200	205	210
Ile Arg Phe Ser Asp	Ser Asn Gly Ser	Val Leu Phe Glu His Pro	215	220	225
Ala Ala Pro Thr Gln	Asp Gly Leu Val	Cys Gly Val Trp Arg Ala	230	235	240
Val Pro Arg Leu Ser	Leu Arg Leu Leu	Arg Ala Glu Gln Leu His	245	250	255
Val Ala Leu Val Thr	Leu Thr His Pro	Ser Gly Glu Val Trp Gly	260	265	270
Pro Leu Ile Arg His	Arg Ala Leu Ala	Ala Glu Thr Phe Ser Ala	275	280	285
Ile Leu Thr Leu Glu	Gly Pro Pro Gln	Gln Gly Val Gly Gly Ile	290	295	300
Thr Leu Leu Thr Leu	Ser Asp Thr Glu	Asp Ser Leu His Phe Leu	305	310	315
Leu Leu Phe Arg Gly	Leu Leu Glu Pro	Arg Ser Gly Gly Leu Thr	320	325	330
Gln Val Pro Leu Arg	Leu Gln Ile Leu	His Gln Gly Gln Leu Leu	335	340	345
Arg Glu Leu Gln Ala	Asn Val Ser Ala	Gln Glu Pro Gly Phe Ala	350	355	360
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Leu	Arg	Ile	Ser	Gly	His	Ile	Ala	Ala	Arg	Lys	Ser	Cys	Asp	Val					
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Val	Ala	Met	Thr	Leu	Glu	Thr	Lys	Pro	Gln	Arg	Arg	Asp	Gln	Arg					
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Thr	Val	Leu	Cys	His	Met	Ala	Gly	Leu	Gln	Pro	Gly	Gly	His	Thr					
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Ala	Val	Gly	Ile	Cys	Pro	Gly	Leu	Gly	Ala	Arg	Gly	Ala	His	Met					
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Leu	Leu	Gln	Asn	Glu	Leu	Phe	Leu	Asn	Val	Gly	Thr	Lys	Asp	Phe					
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Leu	Ala	Gly	Leu	Gly	Gly	Ser	Glu	Gln	Gly	Thr	Val	Thr	Ala	His					
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Gly	Phe	Tyr	Gly	Ser	Glu	Ala	Gln	Gly	Val	Val	Lys	Asp	Leu	Glu					
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Pro	Glu	Leu	Leu	Arg	His	Leu	Ala	Lys	Gly	Met	Ala	Ser	Leu	Met					
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Ile	Thr	Thr	Lys	Gly	Ser	Pro	Arg	Gly	Glu	Leu	Arg	Gly	Gln	Val					
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Ser Ala Ala Pro Pro Val Val Pro Gly Leu Pro Ala Leu Ala Pro	680	685	690
Ala Lys Pro Gly Gly Pro Gly Arg Pro Arg Asp Pro Asn Thr Cys	695	700	705
Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro	710	715	720
Asn Tyr Asp Pro Leu Cys Ser Leu Cys Thr Cys Gln Arg Arg Thr	725	730	735
Val Ile Cys Asp Pro Val Val Cys Pro Pro Pro Ser Cys Pro His	740	745	750
Pro Val Gln Ala Pro Asp Gln Cys Cys Pro Val Cys Pro Glu Lys	755	760	765
Gln Asp Val Arg Asp Leu Pro Gly Leu Pro Arg Ser Arg Asp Pro	770	775	780
Gly Glu Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala	785	790	795
Gly Thr Arg Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys	800	805	810
Cys Ala Val Cys Thr Cys Lys Gly Gly Thr Gly Glu Val His Cys	815	820	825
Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln Pro Val Arg	830	835	840
Val Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly Ser Gly	845	850	855
Ala His Pro Gln Leu Gly Asp Pro Met Gln Ala Asp Gly Pro Arg	860	865	870
Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp	875	880	885
His Pro Ser Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys	890	895	900
Arg Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser	905	910	915
Leu Pro Leu Ser Cys Gly Ser Gly Lys Glu Ser Arg Cys Cys Ser	920	925	930
Arg Cys Thr Ala His Arg Arg Pro Pro Glu Thr Arg Thr Asp Pro	935	940	945
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<212> DNA
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gaaatttaaa atgctagctg ctcaagagtt ttcagtagaa tatttaagaa 2450
ctaattttct gcagctttta gtttgaaaaa aatattttta aaacaaaatt 2500

1. The first step is to identify the problem. This involves understanding the situation and the goals that need to be achieved.

2. The second step is to analyze the problem. This involves breaking down the problem into smaller, more manageable parts.

3. The third step is to develop a plan. This involves determining the steps that need to be taken to solve the problem.

4. The fourth step is to implement the plan. This involves carrying out the steps that have been developed.

5. The fifth step is to evaluate the results. This involves checking to see if the problem has been solved and if the goals have been achieved.

6. The sixth step is to reflect on the process. This involves thinking about what was learned from the experience and how it can be applied in the future.

7. The seventh step is to communicate the results. This involves sharing the findings of the process with others.

8. The eighth step is to document the process. This involves keeping a record of what was done and the results that were achieved.

9. The ninth step is to review the process. This involves looking back at the process and seeing if there are any areas that need to be improved.

10. The tenth step is to celebrate the success. This involves acknowledging the achievements and the hard work that went into solving the problem.

<211> 737

<213> Home

Met Gln Pro Arg Arg Ala Gln Ala Pro Gly Ala Gln Leu Leu Pro
1 5 10 15

Ala Leu Ala Leu Leu Leu Leu Leu Gly Ala Gly Pro Arg Gly
20 25 30

Ser Ser Leu Ala Asn Pro Val Pro Ala Ala Pro Leu Ser Ala Pro
35 40 45

Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr
50 55 60

Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Glu
65 70 75

Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn
80 85 90

Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His
95 100 105

Gly Asn Cys Ser Ser Ser Ser Ser Ser Ser Ser Asp Gly Tyr Leu

110	115	120
Cys Ile Cys Asn Glu Gly Tyr Glu Gly	Pro Asn Cys Glu Gln Ala	
125	130	135
Leu Pro Ser Leu Pro Ala Thr Gly Trp	Thr Glu Ser Met Ala Pro	
140	145	150
Arg Gln Leu Gln Pro Val Pro Ala Thr	Gln Glu Pro Asp Lys Ile	
155	160	165
Leu Pro Arg Ser Gln Ala Thr Val Thr	Leu Pro Thr Trp Gln Pro	
170	175	180
Lys Thr Gly Gln Lys Val Val Glu Met	Lys Trp Asp Gln Val Glu	
185	190	195
Val Ile Pro Asp Ile Ala Cys Gly Asn	Ala Ser Ser Asn Ser Ser	
200	205	210
Ala Gly Gly Arg Leu Val Ser Phe Glu	Val Pro Gln Asn Thr Ser	
215	220	225
Val Lys Ile Arg Gln Asp Ala Thr Ala	Ser Leu Ile Leu Leu Trp	
230	235	240
Lys Val Thr Ala Thr Gly Phe Gln Gln	Cys Ser Leu Ile Asp Gly	
245	250	255
Arg Ser Val Thr Pro Leu Gln Ala Ser	Gly Gly Leu Val Leu Leu	
260	265	270
Glu Glu Met Leu Ala Leu Gly Asn Asn	His Phe Ile Gly Phe Val	
275	280	285
Asn Asp Ser Val Thr Lys Ser Ile Val	Ala Leu Arg Leu Thr Leu	
290	295	300
Val Val Lys Val Ser Thr Cys Val Pro	Gly Glu Ser His Ala Asn	
305	310	315
Asp Leu Glu Cys Ser Gly Lys Gly Lys	Cys Thr Thr Lys Pro Ser	
320	325	330
Glu Ala Thr Phe Ser Cys Thr Cys Glu	Glu Gln Tyr Val Gly Thr	
335	340	345
Phe Cys Glu Glu Tyr Asp Ala Cys Gln	Arg Lys Pro Cys Gln Asn	
350	355	360
Asn Ala Ser Cys Ile Asp Ala Asn Glu	Lys Gln Asp Gly Ser Asn	
365	370	375
Phe Thr Cys Val Cys Leu Pro Gly Tyr	Thr Gly Glu Leu Cys Gln	
380	385	390
Ser Lys Ile Asp Tyr Cys Ile Leu Asp	Pro Cys Arg Asn Gly Ala	
395	400	405

Thr Cys Ile Ser	Ser Leu Ser Gly Phe	Thr Cys Gln Cys Pro Glu	410	415	420
Gly Tyr Phe Gly	Ser Ala Cys Glu Glu Lys Val Asp Pro Cys Ala		425	430	435
Ser Ser Pro Cys	Gln Asn Asn Gly Thr Cys Tyr Val Asp Gly Val		440	445	450
His Phe Thr Cys	Asn Cys Ser Pro Gly Phe Thr Gly Pro Thr Cys		455	460	465
Ala Gln Leu Ile	Asp Phe Cys Ala Leu Ser Pro Cys Ala His Gly		470	475	480
Thr Cys Arg Ser	Val Gly Thr Ser Tyr Lys Cys Leu Cys Asp Pro		485	490	495
Gly Tyr His Gly	Leu Tyr Cys Glu Glu Glu Tyr Asn Glu Cys Leu		500	505	510
Ser Ala Pro Cys	Leu Asn Ala Ala Thr Cys Arg Asp Leu Val Asn		515	520	525
Gly Tyr Glu Cys	Val Cys Leu Ala Glu Tyr Lys Gly Thr His Cys		530	535	540
Glu Leu Tyr Lys	Asp Pro Cys Ala Asn Val Ser Cys Leu Asn Gly		545	550	555
Ala Thr Cys Asp	Ser Asp Gly Leu Asn Gly Thr Cys Ile Cys Ala		560	565	570
Pro Gly Phe Thr	Gly Glu Glu Cys Asp Ile Asp Ile Asn Glu Cys		575	580	585
Asp Ser Asn Pro	Cys His His Gly Gly Ser Cys Leu Asp Gln Pro		590	595	600
Asn Gly Tyr Asn	Cys His Cys Pro His Gly Trp Val Gly Ala Asn		605	610	615
Cys Glu Ile His	Leu Gln Trp Lys Ser Gly His Met Ala Glu Ser		620	625	630
Leu Thr Asn Met	Pro Arg His Ser Leu Tyr Ile Ile Ile Gly Ala		635	640	645
Leu Cys Val Ala	Phe Ile Leu Met Leu Ile Ile Leu Ile Val Gly		650	655	660
Ile Cys Arg Ile	Ser Arg Ile Glu Tyr Gln Gly Ser Ser Arg Pro		665	670	675
Ala Tyr Glu Glu	Phe Tyr Asn Cys Arg Ser Ile Asp Ser Glu Phe		680	685	690
Ser Asn Ala Ile	Ala Ser Ile Arg His Ala Arg Phe Gly Lys Lys				

695

700

705

Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp
 710 715 720

Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys
 725 730 735

Asp Leu

<210> 16

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 16

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 17

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 17

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 18

<211> 508

<212> DNA

<213> Homo Sapien

<400> 18

ctctggaagg tcacggccac aggattccaa cagtgtctccc tcatagatgg 50

acgaaagtgt gacccccctt tcaggctttc agggggactg gtcctcctgg 100

aggagatgct cgccctgggg aataatcact ttattggttt tgtgaatgat 150

tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggatgaagg 200

cagcacctgt gtgccggggg agagtacgc aaatgacttg gagggttcag 250

gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttctgtacc 300

tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350

gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400

aagatgggag caatttcacc tgtgtttgcc ttctgggta tactggagag 450

ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

taggggag 508

<210> 19

<211> 508

<212> DNA

<213> Homo Sapien

<400> 19

ctctggaagg tcacggccac aggattccaa cagtgtccc tcatagatgg 50

acgaaagtgt gacccccctt tcaggctttc agggggactg gtctctctgg 100

aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150

tctgtgacta agtctattgt ggctttgctc ttaactctgg tggatgaagg 200

cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagggttcag 250

gaaaaggaaa atgcaccacg aagccgtcag aggcacttt ttctgtacc 300

tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350

gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400

aagatgggag caatttcacc tgtgtttgcc ttctgggta tactggagag 450

ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

taggggag 508

<210> 20

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 20

ctctggaagg tcacggccac agg 23

<210> 21

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 21

ctcagttcgg ttggcaaagc tctc 24

<210> 22

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 22

cagtgcctccc tcatagatgg acgaaagtgt gacccccctt tcaggcgaga 50

gctttgccaa ccgaactga 69

<210> 23

<211> 1520

<212> DNA

<213> Homo Sapien

<400> 23

gctgagctctg ctgctcctgc tgcctgctgct ccagcctgta acctgtgcct 50

acaccacgcc agggcccccc agagccctca ccacgctggg cggccccaga 100

gcccacacca tgccggggcac ctacgctccc tcgaccacac tcagtagtcc 150

cagcaccag ggctgcaag agcaggcacg ggccctgatg cgggacttcc 200

cgctcgtgga cggccacaac gacctgcccc tggctcctaag gcaggtttac 250

cagaaagggc tacaggatgt taacctgcgc aatttcagct acggccagac 300

cagcctggac aggccttagag atggcctcgt gggcgcccag ttctggtcag 350

cctatgtgcc atgccagacc caggaccggg atgcctgcg cctcaccctg 400

gagcagattg acctatacag ccgcatgtgt gcctcctatt ctgagctgga 450

gcttgtgacc tcggctaaag ctctgaacga cactcagaaa ttggcctgcc 500

tcacgggtgt agaggggtggc cactcgctgg acaatagcct ctccatctta 550

cgtaccttct acatgctggg agtgcgctac ctgacgctca cccacacctg 600

caacacaccc tgggcagaga gctccgctaa gggcgccac tccttctaca 650

acaacatcag cgggctgact gactttggtg agaaggtggt ggcagaaatg 700

aaccgcctgg gcatgatggt agacttatcc catgtctcag atgctgtggc 750

acggcgggcc ctggaagtgt cacaggcacc tgtgatcttc tcccactcgg 800

ctgcccgggg tgtgtgcaac agtgctcgga atgttcctga tgacatcctg 850

cagcttctga agaagaacgg tggcgctcgt atgggtgtctt tgtccatggg 900

agtaatacag tgcaaccat cagccaatgt gtccactgtg gcagatcact 950

tcgaccacat caaggctgtc attggatcca agttcatcgg gattggtgga 1000

gattatgatg gggccggcaa attccctcag gggctggaag acgtgtccac 1050

atacccggtc ctgatagagg agttgctgag tcgtggctgg agtgaggaag 1100

agcttcaggg tgctctcgt ggaaacctgc tgcgggtctt cagacaagtg 1150

gaaaaggtac aggaagaaaa caaatggcaa agccccttgg aggacaagtt 1200
 cccggatgag cagctgagca gttcctgcc ctcgacctc tcacgtctgc 1250
 gtcagagaca gagtctgact tcaggccagg aactcactga gattcccata 1300
 cactggacag ccaagttacc agccaagtgg tcagtctcag agtctctccc 1350
 ccacatggcc ccagtccttg cagttgtggc caccttccca gtccttattc 1400
 tgtggctctg atgaccagc tagtcctgcc agatgtcact gtagcaagcc 1450
 acagacaccc cacaaagttc ccctgttgtg caggcacaaa tatttctga 1500
 aataaatggt ttggacatag 1520

<210> 24
 <211> 433
 <212> PRT
 <213> Homo Sapien

<400> 24
 Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser
 1 5 10 15
 Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
 20 25 30
 Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
 35 40 45
 Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser
 50 55 60
 Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly
 65 70 75
 Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg
 80 85 90
 Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg
 95 100 105
 Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys
 110 115 120
 Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu
 125 130 135
 Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe
 140 145 150
 Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn
 155 160 165
 Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr
 170 175 180

Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala	185	190	195
Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser	200	205	210
Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val	215	220	225
Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg	230	235	240
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly	245	250	255
Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro	260	265	270
Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys	275	280	285
Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp	290	295	300
Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	305	310	315
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu	320	325	330
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	335	340	345
Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu	350	355	360
Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser	365	370	375
Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln	380	385	390
Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala	395	400	405
Lys Trp Ser Val Ser Glu Ser Ser Pro His Met Ala Pro Val Leu	410	415	420
Ala Val Val Ala Thr Phe Pro Val Leu Ile Leu Trp Leu	425	430	

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25
agttctggtc agcctatgtg cc 22

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtgatggtg tctttgtcca tggg 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
ctccaccaat cccgatgaac ttgg 24

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 28
gagcagattg acctcatagc ccgcattgtg gcctcctatt ctgagctgga 50

<210> 29
<211> 1416
<212> DNA
<213> Homo Sapien

<400> 29
aaaacctata aatattccgg attattcata ccgtcccacc atcgggcgcg 50
gatccgcggc cggaattct aaaccaacat gccgggcacc tacgtccct 100
cgaccacact cagtagtccc agcaccagg gcctgcaaga gcaggcacgg 150
gccctgatgc gggacttccc gctogtggac ggccacaacg acctgccct 200
ggtcctaagg caggtttacc agaaagggt acaggatgtt aacctgcgca 250
atttcagcta cggccagacc agcctggaca ggcttagaga tggcctcgtg 300
ggcgcccagt tctggtcagc ctatgtgcca tgccagaccc aggaccggga 350
tgccctgcgc ctcaccctgg agcagattga cctcatacgc ccgatgtgtg 400

cctcctattc tgagctggag cttgtgacct cggctaaagc tctgaacgac 450
 actcagaaat tggcctgcct catcggtgta gaggggtggcc actcgttgga 500
 caatagcctc tccatcttac gtaccttcta catgctggga gtgcgctacc 550
 tgacgctcac ccacacctgc aacacaccct gggcagagag ctccgctaag 600
 ggcgtccact ccttctacaa caacatcagc gggctgactg actttggtga 650
 gaaggtggtg gcagaaatga accgcctggg catgatggta gacttatccc 700
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 gtgatcttct cccactcggc tgccccgggt gtgtgcaaca gtgctcggaa 800
 tgttctgat gacatcctgc agcttctgaa gaagaacggt ggcgtcgtga 850
 tgggtgtctt gtccatggga gtaatacagt gcaacccatc agccaatgtg 900
 tccactgtgg cagatcactt cgaccacatc aaggctgtca ttggatcaa 950
 gttcatcggg attggtggag attatgatgg ggccggcaaa ttccctcagg 1000
 ggttggaaga cgtgtccaca taccgggtcc tgatagagga gttgctgagt 1050
 cgtggctgga gtgaggaaga gcttcagggc gtccttcgtg gaaacctgct 1100
 gcgggtcttc agacaagtgg aaaaggtaca ggaagaaaac aaatggcaaa 1150
 gcccttgga ggacaagttc cgggatgagc agctgagcag ttcttgccac 1200
 tccgacctct cacgtctgcg tcagagacag agtctgactt caggccagga 1250
 actcactgag attcccatac actggacagc caagttacca gccaaagtgt 1300
 cagtctcaga gtcctcccc caccctgaca aaactcacac atgcccaccg 1350
 tgcccagcac ctgaactcct gggggggaccg tcagtcttcc tcttcccccc 1400
 aaaacccaag gacacc 1416

<210> 30

<400> 30

Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly	50	55	60
65	70	75	
Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg	80	85	90
Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg	95	100	105
Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys	110	115	120
Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu	125	130	135
Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe	140	145	150
Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn	155	160	165
Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr	170	175	180
Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala	185	190	195
Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser	200	205	210
Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val	215	220	225
Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg	230	235	240
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly	245	250	255
Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro	260	265	270
Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys	275	280	285
Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp	290	295	300
Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	305	310	315
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu	320	325	330
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	335	340	345



Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
350 355 360
Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
365 370 375
Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
380 385 390
Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
395 400 405
Lys Trp Ser Val Ser Glu Ser Ser Pro His Pro Asp Lys Thr His
410 415 420
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
425 430 435
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
440 445

<210> 31
<211> 1790
<212> DNA
<213> Homo Sapien

<400> 31
cgcccagcga cgtgcgggcg gcttgggccg cgccctcccg cgcccggcct 50
gcgctcccgcg ccttgcgcca ccgcgcgcga gccgcagccc gccgcgcgcc 100
cccggcagcg ccggccccat gcccgcgggc cgccgggggc ccgcgcacca 150
atccgcgcgg cggcgcgcgc cgttgctgcc cctgctgctg ctgctctgcg 200
tcctcggggc gccgcgagcc ggatcaggag ccacacacagc tgtgatcagt 250
ccccaggatc ccacgcttct catcggtctc tccctgctgg ccacctgctc 300
agtgcacgga gacccaccag gagccaccgc cgaggggctc tactggacct 350
tcaacggggc ccgcctgccc cctgagctct cccgtgtact caacgcctcc 400
accttggtctc tggccctggc caacctcaat ggggccaggc agcgggtoggg 450
ggacaacctc gtgtgccacg cccgtgacgg cagcatcctg gctggctcct 500
gcctctatgt tggcctgccc ccagagaaac ccgtcaacat cagctgctgg 550
tccaagaaca tgaaggactt gacctgccgc tggacgccag gggcccacgg 600
ggagaccttc ctccacacca actactccct caagtacaag cttaggtggg 650
atggccagga caacacatgt gaggagtacc acacagtggg gcccactcc 700
tgccacatcc ccaaggacct ggctctcttt acgccctatg agatctgggt 750
ggaggccacc aaccgcctgg gctctgcccg ctccgatgta ctacgctgg 800

[illegible]

<211> 422

<213> Homo Sapien

Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg
1 5 10 15

Pro Pro Pro Leu Leu Pro Leu Leu Leu Leu Leu Cys Val Leu Gly
20 25 30

Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys
50 55 60

SECRET

350 355 360
 Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys
 365 370 375
 Lys His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln
 380 385 390
 Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp
 395 400 405
 Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro
 410 415 420
 Ala Arg

<210> 33
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 33
 cccgcccgcac gtgcacgtga gcc 23

<210> 34
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 34
 tgagccagcc caggaactgc ttg 23

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 35
 caagtgcgct gcaaccctt ttgcatctat ggctccaaga aagccgggat 50

<210> 36
 <211> 1771
 <212> DNA
 <213> Homo Sapien

<400> 36
 cccacgcgtc cgtgtgtgtt agatcgagca accctctaaa agcagtttag 50

E

<211> 300

<213> Homo Sapien

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile
1 5 10 15

Val Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg
20 25 30

Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
35 40 45

His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys
50 55 60

Ser Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu
65 70 75

Thr Ala Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe
80 85 90

Val Val Asp Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys
95 100 105

Lys Val Lys Ala Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn
110 115 120

Ala Gly Val Val Tyr Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro
125 130 135

Gln Ile Glu Lys Thr Phe Glu Val Asn Val Leu Ala His Phe Trp
140 145 150

Thr Thr Lys Ala Phe Leu Pro Ala Met Thr Lys Asn Asn His Gly
155 160 165

His Ile Val Thr Val Ala Ser Ala Ala Gly His Val Ser Val Pro
170 175 180

Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe
185 190 195

32

200	205	210
Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe		
215	220	225
Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu		
230	235	240
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys		
245	250	255
Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu		
260	265	270
Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile		
275	280	285
Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln		
290	295	300

<210> 38
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 38
 ggtgaaggca gaaattggag atg 23

<210> 39
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 39
 atcccatgca tcagcctggt tacc 24

<210> 40
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 40
 gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 41
 <211> 1377
 <212> DNA
 <213> Homo Sapien

<400> 41

gactagtcttct cttggagtctt gggaggagga aagcggagcc ggcagggagc 50
gaaccaggac tggggtgacg gcagggcagg gggcgcttgg ccggggagaa 100
gcgcgggggc tggagcacca ccaactggag ggtccggagt agcgagcgcc 150
ccgaaggagg ccatcgggga gccgggaggg gggactgca gaggaccccg 200
ggtccgggc tcccgtgcc agcgtatga ggccactcct cgtcctgctg 250
ctcctgggcc tggcgcccg ctcgccccca ctggacgaca acaagatecc 300
cagcctctgc ccggggcacc ccggccttcc aggcacgccc ggccaccatg 350
gcagccaggg cttgccgggc cgcgatggcc gcgacggccg cgacggcgcg 400
cccggggctc cgggagagaa aggcgagggc gggaggcccg gactgccggg 450
acctcgaggg gaccccgggc cgcgaggaga ggcgggaccc gcggggccca 500
ccgggcctgc cggggagtgc tcggtgctc cgcgatccgc cttcagcgcc 550
aagcgctccg agagccgggt gcctccgccc tctgacgcac ccttgccctt 600
cgaccgcgtg ctggtgaacg agcagggaca ttacgacgcc gtcaccggca 650
agttcacctg ccaggtgcct ggggtctact acttcgccgt ccatgccacc 700
gtctaccggg ccagcctgca gtttgatctg gtgaagaatg gcgaatccat 750
tgctcttttc ttccagtttt tcggggggtg gcccaagcca gcctcgctct 800
cggggggggc catggtgagg ctggagcctg aggaccaagt gtgggtgcag 850
gtgggtgtgg gtgactacat tggcatctat gccagcatca agacagacag 900
caccttctcc ggatttctgg tgtactccga ctggcacagc tccccagtct 950
ttgcttagtg cccactgcaa agtgagctca tgctctcact cctagaagga 1000
gggtgtgagg ctgacaacca ggtcatccag gagggtggc cccctggaa 1050
tattgtgaat gactagggag gtggggtaga gcactctccg tcctgctgct 1100
ggcaaggaaat gggaacagtg gctgtctgcg atcaggtctg gcagcatggg 1150
gcagtggctg gatttctgcc caagaccaga ggagtgtgct gtgctggcaa 1200
gtgtaagtcc ccagttgct ctggtccagg agcccaagggt ggggtgctct 1250
cttctgggc ctctgcttct ctggatcctc cccacccct cctgctctg 1300
gggccggccc ttttctcaga gatcactcaa taaacctaa aacctcata 1350
aaaaaaaaa aaaaaaaaaa aaaaaaa 1377

<210> 42

<211> 243
 <212> PRT
 <213> Homo Sapien

<400> 42

Met	Arg	Pro	Leu	Leu	Val	Leu	Leu	Leu	Leu	Gly	Leu	Ala	Ala	Gly	1	5	10	15
Ser	Pro	Pro	Leu	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro	Gly	20	25	30		
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly	35	40	45	
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly	50	55	60	
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly	65	70	75	
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly	80	85	90	
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala	95	100	105	
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp	110	115	120	
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His	125	130	135	
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val	140	145	150	
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln	155	160	165	
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln	170	175	180	
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala	185	190	195	
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly	200	205	210	
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser	215	220	225	
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro	230	235	240	
Val	Phe	Ala																

<210> 43
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 43
 tacaggccca gtcaggacca gggg 24

 <210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 44
 agccagcctc gctctcgg 18

 <210> 45
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 45
 gtctgcgatc aggtctgg 18

 <210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 46
 gaaagaggca atggattcgc 20

 <210> 47
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 47
 gacttacact tgccagcaca gcac 24

 <210> 48
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49

<211> 1876

<212> DNA

<213> Homo Sapien

<400> 49

ctcttttgtc caccagccca gcctgactcc tggagattgt gaatagctcc 50
atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100
aactgacggg cccaacagac ccatgctgca tccagagacc tcccctggcc 150
gggggcatct cctggctgtg ctcttgccc tccttggcac cacctgggca 200
gaggtgtggc caccagct gcaggagcag gctccgatgg ccggagccct 250
gaacaggaag gagagtttct tgctcctctc cctgcacaac cgcctgcgca 300
gctgggtcca gcccctgctg gctgacatgc ggaggctgga ctggagtgc 350
agcctggccc aactggctca agccaggga gccctctgtg gaatcccaac 400
cccgagcctg gcctccggcc tgtggcgcc cctgcaagtg ggctggaaca 450
tgcagctgct gcccggggc ttggcgctct ttgttgaagt ggtcagccta 500
tggtttgcag aggggcagcg gtacagccac gggcaggag agtgtgctcg 550
caacgccacc tgacccact acacgcagct cgtgtgggccc acctcaagcc 600
agctgggctg tgggcggcac ctgtgctctg caggccagac agcgatagaa 650
gcctttgtct gtgcctactc ccccgaggc aactgggagg tcaacgggaa 700
gacaatcatc cctataaga agggcgctg gtgttcgctc tgcacagcca 750
gtgtctcagg ctgcttcaaa gcctgggacc atgcaggggg gctctgtgag 800
gtccccagga atccttgtcg catgagctgc cagaaccatg gacgtctcaa 850
catcagcacc tgccactgcc actgtccccc tggctacacg ggcagatact 900
gccaaagtgc gtgcagcctg cagtgtgtgc acggccggtt ccgggaggag 950
gagtgtcgt gcgtctgtga catcggtac gggggagccc agtgtgccac 1000
caaggtgcat ttcccttcc acacctgtga cctgaggatc gacggagact 1050
gcttcaggt gtcttcagag gcagacacct attacagagc caggatgaaa 1100
tgtcagagga aaggcggggt gctggcccag atcaagagcc agaaagtgc 1150

ggacatcctc gccttctatc tgggcccgcct ggagaccacc aacgaggtga 1200
 ctgacagtga cttcgagacc aggaacttct ggatcgggct cacctacaag 1250
 accgccaagg actccttcog ctggggccaca ggggagcacc aggccttcac 1300
 cagttttgcc tttgggcagc ctgacaacca cgggctgggtg tggctgagtg 1350
 ctgccatggg gtttggaac tgcgtggagc tgcaggcttc agctgccttc 1400
 aactggaacg accagcgtg caaaaccoga aaccgttaca tctgccagtt 1450
 tgcccaggag cacatctccc ggtggggccc agggctctga ggctgacca 1500
 catggctccc tgcctgccc tgggagcacc ggctctgctt acctgtctgc 1550
 ccacctgtct ggaacaaggg ccaggttaag accacatgcc tcatgtccaa 1600
 agaggtctca gaccttgac aatgccagaa gttgggcaga gagaggcagg 1650
 gaggccagtg agggccaggg agtgagtgtt agaagaagct ggggcccttc 1700
 gcctgctttt gattgggaag atgggcttca attagatggc gaaggagagg 1750
 acaccgccag tggtcacaaa aggctgctct cttccacctg gccagaccc 1800
 tgtggggcag cggagcttcc ctgtggcatg aacccacgg ggtattaaat 1850
 tatgaatcag ctgaaaaaaaa aaaaaa 1876

<210> 50
 <211> 455
 <212> PRT
 <213> Homo Sapien

<400> 50
 Met Leu His Pro Glu Thr Ser Pro Gly Arg Gly His Leu Leu Ala
 1 5 10 15
 Val Leu Leu Ala Leu Leu Gly Thr Thr Trp Ala Glu Val Trp Pro
 20 25 30
 Pro Gln Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg
 35 40 45
 Lys Glu Ser Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser
 50 55 60
 Trp Val Gln Pro Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser
 65 70 75
 Asp Ser Leu Ala Gln Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly
 80 85 90
 Ile Pro Thr Pro Ser Leu Ala Ser Gly Leu Trp Arg Thr Leu Gln
 95 100 105
 Val Gly Trp Asn Met Gln Leu Leu Pro Ala Gly Leu Ala Ser Phe

	110	115	120
Val Glu Val Val Ser Leu Trp Phe Ala Glu Gly Gln Arg Tyr Ser	125	130	135
His Ala Ala Gly Glu Cys Ala Arg Asn Ala Thr Cys Thr His Tyr	140	145	150
Thr Gln Leu Val Trp Ala Thr Ser Ser Gln Leu Gly Cys Gly Arg	155	160	165
His Leu Cys Ser Ala Gly Gln Thr Ala Ile Glu Ala Phe Val Cys	170	175	180
Ala Tyr Ser Pro Gly Gly Asn Trp Glu Val Asn Gly Lys Thr Ile	185	190	195
Ile Pro Tyr Lys Lys Gly Ala Trp Cys Ser Leu Cys Thr Ala Ser	200	205	210
Val Ser Gly Cys Phe Lys Ala Trp Asp His Ala Gly Gly Leu Cys	215	220	225
Glu Val Pro Arg Asn Pro Cys Arg Met Ser Cys Gln Asn His Gly	230	235	240
Arg Leu Asn Ile Ser Thr Cys His Cys His Cys Pro Pro Gly Tyr	245	250	255
Thr Gly Arg Tyr Cys Gln Val Arg Cys Ser Leu Gln Cys Val His	260	265	270
Gly Arg Phe Arg Glu Glu Glu Cys Ser Cys Val Cys Asp Ile Gly	275	280	285
Tyr Gly Gly Ala Gln Cys Ala Thr Lys Val His Phe Pro Phe His	290	295	300
Thr Cys Asp Leu Arg Ile Asp Gly Asp Cys Phe Met Val Ser Ser	305	310	315
Glu Ala Asp Thr Tyr Tyr Arg Ala Arg Met Lys Cys Gln Arg Lys	320	325	330
Gly Gly Val Leu Ala Gln Ile Lys Ser Gln Lys Val Gln Asp Ile	335	340	345
Leu Ala Phe Tyr Leu Gly Arg Leu Glu Thr Thr Asn Glu Val Thr	350	355	360
Asp Ser Asp Phe Glu Thr Arg Asn Phe Trp Ile Gly Leu Thr Tyr	365	370	375
Lys Thr Ala Lys Asp Ser Phe Arg Trp Ala Thr Gly Glu His Gln	380	385	390
Ala Phe Thr Ser Phe Ala Phe Gly Gln Pro Asp Asn His Gly Leu	395	400	405

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg
440 445 450

Trp Gly Pro Gly Ser
455

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 51
aggaacttct ggatcgggct cacc 24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 52
gggtctgggc caggtggaag agag 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
gccaaaggact ccttccgctg ggccacaggg gagcaccagg ccttc 45

<210> 54
<211> 2331
<212> DNA
<213> Homo Sapien

<400> 54
cggacgcgtg ggctgggagc tgcaaagcgt gtcccgcagg gtccccgagc 50
gtcccgcagg ctcgccccgc catgctcctg ctgctggggc tgtgacctggg 100
gctgtccctg tgtgtggggg cgaggaaga ggagcagagc tggggccact 150
cttcggagca ggatggactc aggggtccga ggcaagtcag actgttgcag 200

aggctgaaaa ccaaaccctt gatgacagaa ttctcagtga agtctacat 250
 catttcccgat tatgccttca ctacgggttc ctgcagaatg ctgaacagag 300
 cttctgaaga ccaggacatt gagttccaga tgcagattcc agctgcagct 350
 ttcattacca acttcactat gcttatttga gacaagggtg atcagggcga 400
 aattacagag agagaaaaga agagtgggtg tagggtaaaa gagaaaagga 450
 ataaaaccac agaagaaaat ggagagaagg ggactgaaat attcagagct 500
 tctgcagtga ttcccagcaa ggacaaagcc gcctttttcc tgagttatga 550
 ggagcttctg cagaggcgcc tgggcaagta cgagcacagc atcagcgtgc 600
 ggccccagca gctgtccggg aggctgagcg tggacgtgaa tatcctggag 650
 agcgcgggca tgcateccct ggaggtgctg ccgcttcaca acagcaggca 700
 gaggggcagt gggcgcgggg aagatgattc tgggcctccc ccatctactg 750
 tcattaacca aaatgaaaca ttgtccaaca taatttttaa acctactgta 800
 gtacaacaag ccaggattgc ccagaatgga attttgggag actttatcat 850
 tagatatgac gtcaatagag aacagagcat tggggacatc caggttctaa 900
 atggctatct tgtgcaactac ttgtctcta aagaccttcc tcctttacc 950
 aagaatgtgg tattcgtgct tgacagcagt gcttctatgg tgggaaccaa 1000
 actccggcag accaaggatg cctcttcac aattctccat gacctccgac 1050
 cccaggaccg ttctcagtac attggatttt ccaaccggat caaagtatgg 1100
 aaggaccact tgatatcagt cactccagac agcatcaggg atgggaaagt 1150
 gtacattcac catatgtcac cactggagg cacagacatc aacggggccc 1200
 tgcagagggc catcaggctc ctcaacaagt acgtggccca cagtggcatt 1250
 ggagaccgga gctgtccct catcgtcttc ctgacggatg ggaagccac 1300
 ggtcggggag acgcacacc tcaagatcct caacaacacc cgagaggccg 1350
 cccgaggcca agtctgcatc ttaccattg gcatcggcaa cgacgtggac 1400
 ttccaggtgc tggagaaact gtcgctggag aactgtggcc tcacacggcg 1450
 cgtgcacgag gaggaggacg caggctcgca gctcatcggg ttctacgatg 1500
 aaatcaggac cccgctctc tctgacatcc gcatcgatta tccccacg 1550
 tcagtgggtg aggccaccaa gacctgttc cccaactact tcaacggctc 1600
 ggagatcatc attgcgggga agctgggtga caggaagctg gatcacctgc 1650

[illegible]

<213> Homo Sapien

Val Tyr Gln Gly Glu Ile Thr Glu Arg Glu Lys Lys Ser Gly Asp
110 115 120

Arg Val Lys Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu	125	130	135
Lys Gly Thr Glu Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys	140	145	150
Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg	155	160	165
Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val Arg Pro Gln Gln	170	175	180
Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu Glu Ser Ala	185	190	195
Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser Arg Gln	200	205	210
Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro Ser	215	220	225
Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys	230	235	240
Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu	245	250	255
Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile	260	265	270
Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala	275	280	285
Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu	290	295	300
Asp Ser Ser Ala Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys	305	310	315
Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg	320	325	330
Phe Ser Ile Ile Gly Phe Ser Asn Arg Ile Lys Val Trp Lys Asp	335	340	345
His Leu Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Lys Val	350	355	360
Tyr Ile His His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly	365	370	375
Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His	380	385	390
Ser Gly Ile Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu Thr	395	400	405
Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu			

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
gtgggaacca aactcggca gacc 24

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
cacatcgagc gtctctgg 18

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 58
agccgtect tctccggttc atcg 24

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
tggaaggacc acttgatata agtcactcca gacagcatca gggatggg 48

<210> 60
<211> 1413
<212> DNA
<213> Homo Sapien

<400> 60
cggacgcgtg gggcgccga catggcgagt gtagtgctgc cgagcggatc 50
ccagtgtgcg gcggcagcgg cggcggcggc gcctcccggg ctccggcttc 100
tgctgttget cttctccgcc gcggcactga tccccacagg tgatgggcag 150
aatctgttta cgaaagacgt gacagtgatc gagggagagg ttgcgaccat 200

cagttgccaa gtcaataaga gtgacgactc tgtgattcag ctactgaatc 250
ccaacaggca gaccatttat ttcagggact tcaggccttt gaaggacagc 300
aggtttcagt tgctgaattt ttctagcagt gaactcaaag tatcattgac 350
aaacgtctca atttctgatg aaggaagata cttttgccag ctctataaccg 400
atccccaca ggaaagtac accaccatca cagtcctggg cccaccacgt 450
aatctgatga tcgatatcca gaaagacact gcggtggaag gtgaggagat 500
tgaagtcaac tgcactgcta tggccagcaa gccagccacg actatcaggt 550
ggttcaaagg gaacacagag ctaaaaggca aatcggaggt ggaagagtgg 600
tcagacatgt aactgtgac cagtcagctg atgctgaagg tgcacaagga 650
ggacgatggg gtcccagtga tctgccaggt ggagcaccct gcggtcactg 700
gaaacctgca gaccagcgg tatctagaag tacagtataa gcctcaagtg 750
cacattcaga tgacttatcc tctacaaggc ttaaccggg aaggggacgc 800
gcttgagtta acatgtgaag ccatcgggaa gcccagcct gtgatggtaa 850
cttgggtgag agtcgatgat gaaatgcctc aacacgccgt actgtctggg 900
cccaacctgt tcatcaataa cctaaacaaa acagataatg gtacataaccg 950
ctgtgaagct tcaaacatag tggggaaagc tcaactcgat tatatgtctg 1000
atgtatacga tccccccaca actatccctc ctcccacaac aaccaccacc 1050
accaccacca ccaccaccac caccatcctt accatcatca cagattcccg 1100
agcaggtgaa gaaggctcga tcagggcagt ggatcatgcc gtgatcggtg 1150
gcgtcgtggc ggtgggtggg ttgccatgc tgtgcttgc catcattctg 1200
gggcgctatt ttgccagaca taaagggtaca tacttcactc atgaagccaa 1250
aggagccgat gacgcagcag acgcagacac agctataatc aatgcagaag 1300
gaggacagaa caactccgaa gaaaagaaag agtacttcat ctagatcagc 1350
ctttttgttt caatgaggtg tccaactggc cctattttaga tgataaagag 1400
acagtgatat tgg 1413

<210> 61
<211> 440
<212> PRT
<213> Homo Sapien

<400> 61
Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala
1 5 10 15

Ala Ala Ala Ala Ala	Pro Pro Gly Leu Arg	Leu Leu Leu Leu Leu	20	25	30
Phe Ser Ala Ala Ala	Leu Ile Pro Thr Gly Asp	Gly Gln Asn Leu	35	40	45
Phe Thr Lys Asp Val	Thr Val Ile Glu Gly Glu	Val Ala Thr Ile	50	55	60
Ser Cys Gln Val Asn	Lys Ser Asp Asp Ser	Val Ile Gln Leu Leu	65	70	75
Asn Pro Asn Arg Gln	Thr Ile Tyr Phe Arg	Asp Phe Arg Pro Leu	80	85	90
Lys Asp Ser Arg Phe	Gln Leu Leu Asn Phe	Ser Ser Ser Glu Leu	95	100	105
Lys Val Ser Leu Thr	Asn Val Ser Ile Ser	Asp Glu Gly Arg Tyr	110	115	120
Phe Cys Gln Leu Tyr	Thr Asp Pro Pro Gln	Glu Ser Tyr Thr Thr	125	130	135
Ile Thr Val Leu Val	Pro Pro Arg Asn Leu	Met Ile Asp Ile Gln	140	145	150
Lys Asp Thr Ala Val	Glu Gly Glu Glu Ile	Glu Val Asn Cys Thr	155	160	165
Ala Met Ala Ser Lys	Pro Ala Thr Thr Ile	Arg Trp Phe Lys Gly	170	175	180
Asn Thr Glu Leu Lys	Gly Lys Ser Glu Val	Glu Glu Trp Ser Asp	185	190	195
Met Tyr Thr Val Thr	Ser Gln Leu Met Leu	Lys Val His Lys Glu	200	205	210
Asp Asp Gly Val Pro	Val Ile Cys Gln Val	Glu His Pro Ala Val	215	220	225
Thr Gly Asn Leu Gln	Thr Gln Arg Tyr Leu	Glu Val Gln Tyr Lys	230	235	240
Pro Gln Val His Ile	Gln Met Thr Tyr Pro	Leu Gln Gly Leu Thr	245	250	255
Arg Glu Gly Asp Ala	Leu Glu Leu Thr Cys	Glu Ala Ile Gly Lys	260	265	270
Pro Gln Pro Val Met	Val Thr Trp Val Arg	Val Asp Asp Glu Met	275	280	285
Pro Gln His Ala Val	Leu Ser Gly Pro Asn	Leu Phe Ile Asn Asn	290	295	300
Leu Asn Lys Thr Asp	Asn Gly Thr Tyr Arg	Cys Glu Ala Ser Asn			

305	310	315
Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp		
320	325	330
Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr		
335	340	345
Thr Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg		
350	355	360
Ala Gly Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile		
365	370	375
Gly Gly Val Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu		
380	385	390
Ile Ile Leu Gly Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe		
395	400	405
Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr		
410	415	420
Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser Glu Glu Lys		
425	430	435
Lys Glu Tyr Phe Ile		
440		

- <210> 62
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 62
- ggcttctgct gttgctcttc tccg 24
- <210> 63
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 63
- gtacactgtg accagtcagc 20
- <210> 64
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 64
atcatcacag attccccgagc 20

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaccttcca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

<400> 68
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DECLARATION OF INTEREST The authors have nothing to disclose.

<211> 598

<213> Hom

Met Cys

1

20

35

50

65

80

95

51

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Leu	Phe	Ser	Arg	Leu	Arg	Asn	Leu	His	Asp	Leu	Asp	Val	Ser	Asp
				140					145					150
Asn	Gln	Leu	Glu	Arg	Val	Pro	Pro	Val	Ile	Arg	Gly	Leu	Arg	Gly
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Leu	Thr	Arg	Leu	Arg	Leu	Ala	Gly	Asn	Thr	Arg	Ile	Ala	Gln	Leu
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Arg	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Ala	Ala	Leu	Gln	Glu	Leu	Asp
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Val	Ser	Asn	Leu	Ser	Leu	Gln	Ala	Leu	Pro	Gly	Asp	Leu	Ser	Gly
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Leu	Phe	Pro	Arg	Leu	Arg	Leu	Leu	Ala	Ala	Ala	Arg	Asn	Pro	Phe
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Asn	Cys	Val	Cys	Pro	Leu	Ser	Trp	Phe	Gly	Pro	Trp	Val	Arg	Glu
				230					235					240
Ser	His	Val	Thr	Leu	Ala	Ser	Pro	Glu	Glu	Thr	Arg	Cys	His	Phe
				245					250					255
Pro	Pro	Lys	Asn	Ala	Gly	Arg	Leu	Leu	Leu	Glu	Leu	Asp	Tyr	Ala
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Asp	Phe	Gly	Cys	Pro	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Val	Pro	Thr
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Thr	Arg	Pro	Val	Val	Arg	Glu	Pro	Thr	Ala	Leu	Ser	Ser	Ser	Leu
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Ser	Pro	Pro	Ser	Thr	Ala	Pro	Pro	Thr	Val	Gly	Pro	Val	Pro	Gln
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Pro	Gln	Asp	Cys	Pro	Pro	Ser	Thr	Cys	Leu	Asn	Gly	Gly	Thr	Cys
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His	Leu	Gly	Thr	Arg	His	His	Leu	Ala	Cys	Leu	Cys	Pro	Glu	Gly
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Phe	Thr	Gly	Leu	Tyr	Cys	Glu	Ser	Gln	Met	Gly	Gln	Gly	Thr	Arg
				365					370					375
Pro	Ser	Pro	Thr	Pro	Val	Thr	Pro	Arg	Pro	Pro	Arg	Ser	Leu	Thr
				380					385					390
Leu	Gly	Ile	Glu	Pro	Val	Ser	Pro	Thr	Ser	Leu	Arg	Val	Gly	Leu
				395					400					405

Gln Arg Tyr Leu	Gln Gly Ser Ser Val	Gln Leu Arg Ser Leu Arg
410	415	420
Leu Thr Tyr Arg	Asn Leu Ser Gly Pro	Asp Lys Arg Leu Val Thr
425	430	435
Leu Arg Leu Pro	Ala Ser Leu Ala Glu	Tyr Thr Val Thr Gln Leu
440	445	450
Arg Pro Asn Ala	Thr Tyr Ser Val Cys	Val Met Pro Leu Gly Pro
455	460	465
Gly Arg Val Pro	Glu Gly Glu Glu Ala	Cys Gly Glu Ala His Thr
470	475	480
Pro Pro Ala Val	His Ser Asn His Ala	Pro Val Thr Gln Ala Arg
485	490	495
Glu Gly Asn Leu	Pro Leu Leu Ile Ala	Pro Ala Leu Ala Ala Val
500	505	510
Leu Leu Ala Ala	Leu Ala Ala Val Gly	Ala Ala Tyr Cys Val Arg
515	520	525
Arg Gly Arg Ala	Met Ala Ala Ala Ala	Gln Asp Lys Gly Gln Val
530	535	540
Gly Pro Gly Ala	Gly Pro Leu Glu Leu	Glu Gly Val Lys Val Pro
545	550	555
Leu Glu Pro Gly	Pro Lys Ala Thr Glu	Gly Gly Gly Glu Ala Leu
560	565	570
Pro Ser Gly Ser	Glu Cys Glu Val Pro	Leu Met Gly Phe Pro Gly
575	580	585
Pro Gly Leu Gln	Ser Pro Leu His Ala	Lys Pro Tyr Ile
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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

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<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

cggttctggg gacgttaggg ctcg 24

<210> 72

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

ctgcccaccg tccacctgcc tcaat 25

<210> 73

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 73

aggactgccc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 74

acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75

<211> 1077

<212> DNA

<213> Homo Sapien

<400> 75

ggcactagga caaccttctt cctttctgca ccaactgccc tacccttacc 50

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gccggctgca ggggacagga ggccccctcc agaatgggga agggatatcc 350

tggcagagtc tcccggagca gagttccgat gccctggaag cctgggagaa 400

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

2. Once the problem is identified, the next step is to define the objectives and goals of the project. This helps to clarify what needs to be achieved and provides a clear direction for the team.

3. The third step is to develop a plan or strategy to address the problem. This involves breaking down the problem into smaller, manageable tasks and determining the resources needed to complete each task.

4. The fourth step is to implement the plan. This involves putting the strategy into action and monitoring progress along the way. It is important to stay flexible and make adjustments as needed.

5. The final step is to evaluate the results of the project. This involves assessing whether the objectives were met and identifying any lessons learned for future projects.

<211> 250

<213> Homo Sapien

Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro
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Gly Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala
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Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala
35 40 45

Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg
50 55 60

Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
65 70 75

Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala
80 85 90

Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala
95 100 105

Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His Leu
110 115 120

SECRET

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tgccgtcttc cggaagacct tttcccttgc tctgttttct tcaccgagtc 200

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<211> 281

<212> PRT

<213> Homo Sapien

<400> 78

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 20 25 30

Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
 35 40 45

Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr
 50 55 60

Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
 65 70 75

Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro
 80 85 90

Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
 95 100 105

Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly

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Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly		
125	130	135
Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val		
140	145	150
Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val		
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met		
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe		
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His		
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val		
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu		
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg		
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe		
260	265	270
Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro		
275	280	

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

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<210> 80
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 80
 ctgaagaagt agaggccggg cacg 24

<210> 81

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
cccgggtgctt ggcgtgctgt gaccccggtta cctccatgta cccgg 45

<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

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<211> 431

<212> PRT

<213> Homo Sapien

<400> 83

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Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu	35	40	45
Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln	50	55	60
Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly	65	70	75
Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala	80	85	90
Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala	95	100	105
Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile	110	115	120
Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu	125	130	135
Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val	140	145	150
Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp	155	160	165
Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp	170	175	180
His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu	185	190	195
Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser	200	205	210
Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala	215	220	225
Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala	230	235	240
Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr	245	250	255
Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro	260	265	270
Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr	275	280	285
Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr	290	295	300
Ala Val Leu Thr Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly			

TOFESQ "4464660

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Asn Thr Gly Asn Val Tyr Asn Pro Thr	Ala Leu Ser Met Ser Asn	
335	340	345
Val Glu Ser Ser Thr Met Asn Lys Thr	Ala Ser Trp Glu Gly Arg	
350	355	360
Glu Ala Ser Pro Gly Ser Ser Ser Gln	Gly Ser Val Pro Glu Asn	
365	370	375
Gln Tyr Gly Leu Pro Phe Glu Lys Trp	Leu Leu Ile Gly Ser Leu	
380	385	390
Leu Phe Gly Val Leu Phe Leu Val Ile	Gly Leu Val Leu Leu Gly	
395	400	405
Arg Ile Leu Ser Glu Ser Leu Arg Arg	Lys Arg Tyr Ser Arg Leu	
410	415	420
Asp Tyr Leu Ile Asn Gly Ile Tyr Val	Asp Ile	
425	430	

- <210> 84
- <211> 30
- <212> DNA
- <213> Artificial Sequence
- <220>
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- <400> 84
- agggaggatt atccttgacc tttgaagacc 30
- <210> 85
- <211> 18
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 85
- gaagcaagtg cccagctc 18
- <210> 86
- <211> 18
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- <213> Artificial Sequence
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- <400> 86
- cgggtccctg ctcttttg 18

<210> 87
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caccgtagct gggagcgcac tcac 24

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agtgttaagtc aagctccc 18

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<213> Homo Sapien

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gtcttcgcct ccttggtgtgc ctggtattcg gggtagctgc tcgcagagct 100
cattccagat gcacccctgt ccagtgtgc ctatagcatc cgcagcatcg 150
gggagaggcc tgtcctcaaa gctccagtcc ccaaaaaggca aaaatgtgac 200
cactggactc cctgcccac tcacacctat gcctacaggt tactcagcgg 250
agggtggcaga agcaagtacg ccaaaaatctg ctttgaggat aacctactta 300
tgggagaaca gctgggaaat gttgccagag gaataaacat tgccattgtc 350
aactatgtaa ctgggaatgt gacagcaaca cgatgttttg atatgtatga 400
aggcgataac tctggaccga tgacaaagtt tattcagagt gctgctccaa 450
aatccctgct cttcatggtg acctatgacg acggaagcac aagactgaat 500

aacgatgccca agaatgccat agaagcactt ggaagtaaag aaatcaggaa 550
 catgaaattc aggtctagct gggatatttat tgcagcaaaa ggcttgggaac 600
 tcccttccga aattcagaga gaaaagatca accactctga tgctaagaac 650
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 caaagaacga agctgacact gcagggtcct gagtaaatgt gttctgtata 750
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 gcccatatatt gatgagtatt ttgggtttgt tgtaaaccac tgaacatttg 850
 ctagttgtat caaatcttgg tacgcagtat tttataacca gtattttatg 900
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 aaaaaaa 957

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 <212> PRT
 <213> Homo Sapien

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 Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu
 20 25 30
 Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg
 35 40 45
 Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
 50 55 60
 Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
 65 70 75
 Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile
 80 85 90
 Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
 95 100 105
 Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
 110 115 120
 Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser
 125 130 135
 Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
 140 145 150
 Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
 155 160 165

Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser Lys Glu Ile Arg
 170 175 180
 Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
 185 190 195
 Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn His Ser
 200 205 210
 Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile Gln
 215 220 225
 Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
 230 235

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<210> 93

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<400> 93

aggcttggaa ctcccttc 18

<210> 94

<211> 24

<212> DNA

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<220>

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aagattcttg agcgattcca gctg 24

<210> 95

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ccaacctcag cttccgcctc tacga 25

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catccagget cgccactg 18

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68

TCF80" 445-450

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tggcccagct gacgagccct 20

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<400> 108

tggctcccag cttggaaga 19

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<211> 21

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<213> Artificial Sequence

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ggattctaat acgactcact atagggccgc cccgccacct cct 43

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

ctatgaaatt aaccctcact aaagggactc gagacaccac ctgaccca 48

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ggattctaatac gactcact atagggccca aggaaggcag gagactct 48

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ctatgaaatt aaccctcact aaagggaacta ggggggtggga atgaaaaag 48

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